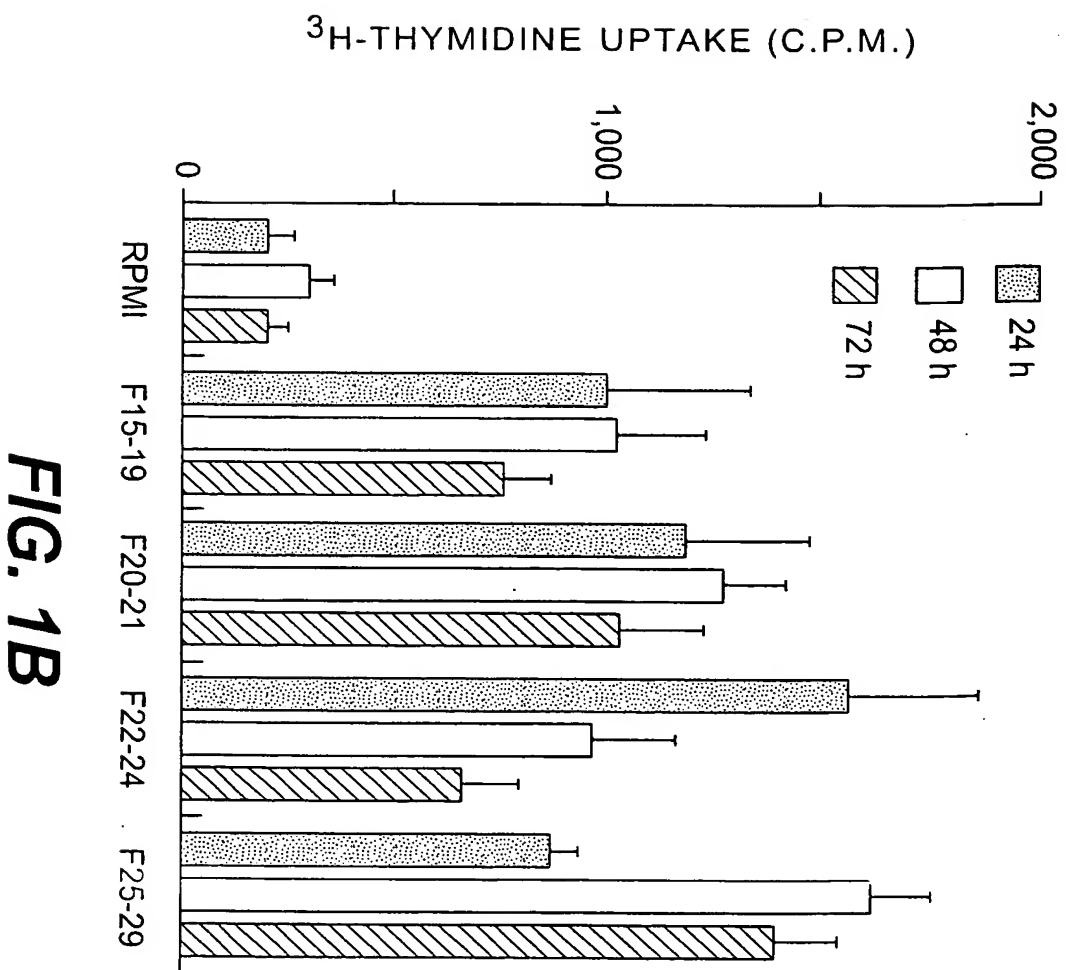
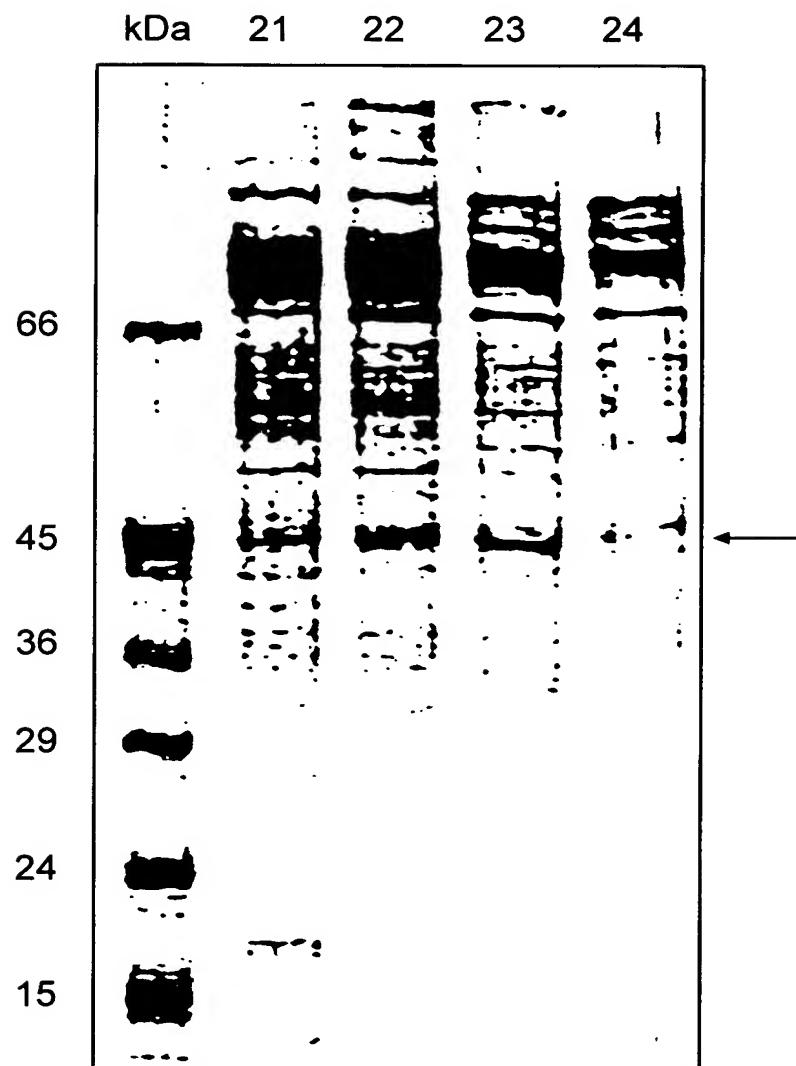


**FIG. 1A**



**FIG. 1B**

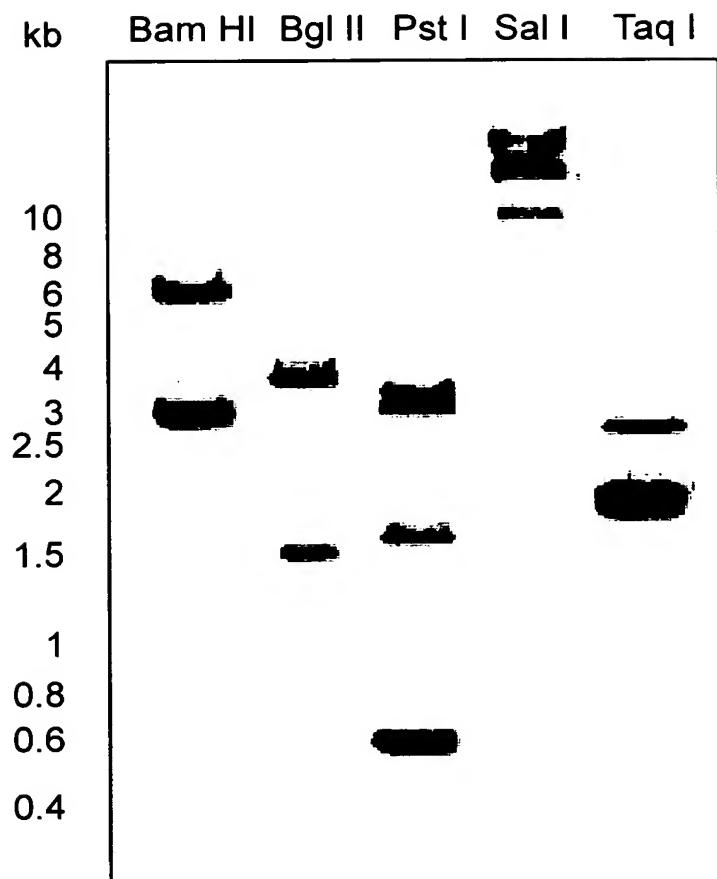
HPLC FRACTIONS



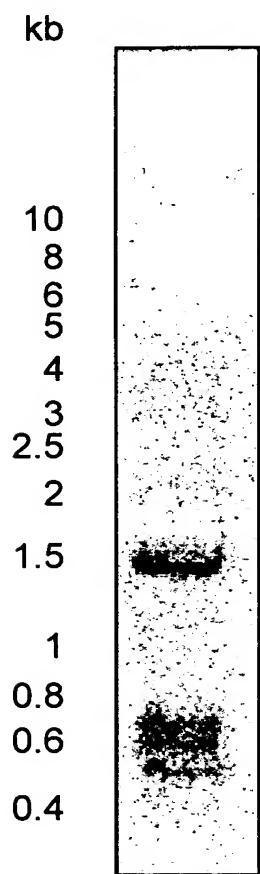
**FIG. 1C**

TC	MRKSVCVKQFFFSAFPFFFFCVFPLISRTQKQYKIIKGEKKKNQRANRREHQKREIMRFKKS	75
CS	-----MKFSKG	6
Pa	-----MQR	3
TC	FTCIDMHTGEAARIWTSGLPHIPGSNMAEKAYLQENMDYLRRGIMLEPRGHDDMFGAFLDPFEEGADLGWVF	150
CS	IHAIDSHTMGEPTRIWVGGIPOQINGETMADKKYLEDNLVDYVRTALMHEPRGHNDMFGSIITSSNNKEADFGIIF	81
Pa	IRIDSHTGGEPTRLVIGGFPLGQGDMERRRLIGERHDAMRAACILEPRGSDVLVGLCAPDPEACAGVIF	78
TC	MDTGGYLNMCGHNSIAAVTAAWETGIVSVPAKATNVVVLDTPAGLVRGTAHLOSGTESEVNASIINVPSFLYQ	225
CS	MDGGGYLNMCGHGSIGAATVAEVETGMVEMVEPVTNIN--MEAPAGLIKAKVMVEN--EVKVEVSITNVPSFLYQ	151
Pa	FNNSGYLGMCGHGTIGLVALASLAHLGRIGPGV----HRIETPVGEVEATH-----EDGSVSVRNVPAYRYR	140
TC	ODVVVVLPKPYGEVRVDIAFGGNFFAIVPAEQLGIDISVONLSRLOEAGELLRITEINRSVKVOHPOLPHINTVDC	300
CS	EDAKLEVPSLNKTITFDISFGGSSFAIHAKELGVKVETSQDVLLKLGIEIRDLINEKIKVQHPELEHIKTVDL	226
Pa	RQSVVEVPGI--GRVSGDIAMGGNNWEFLVAGH--GQLAGDNLDALTAYTWAVOALDD---QDIRGEDGAIIDH	208
TC	VEIYGPPTNPEANYKNVVFIGNMROADR SPCGT GTSAKMATLYAKGQLRIGETFYYESILGSLFQGRV--LGEE	371
CS	VEIYDEPSNPEATYKNVWFQGQVDR SPCGT GTSAKLATLYKKGHLKIDEKFVYESITGTMFKGRV--LEET	297
Pa	IELFAD--DPHADSRNFVLCPGKAYDR SPCGT GTSAKLACLAADGKLIPGQWPWRQASVIGSQFEGRYEWLDQ	279
TC	RIPGVKVPVTKDAEEMLVVTAETGKAFIGFNTMLFDPTDPFKNGFTLKQ* 423	
CS	KVGEFD-----AIIPETGGAYITGFNFHVVIDPEDPLIKYGFV*-- 335	
Pa	PGGPPIVPTIRGRAHVSAEATLLADDDPFANGIRR*----- 314	

**FIG. 2**

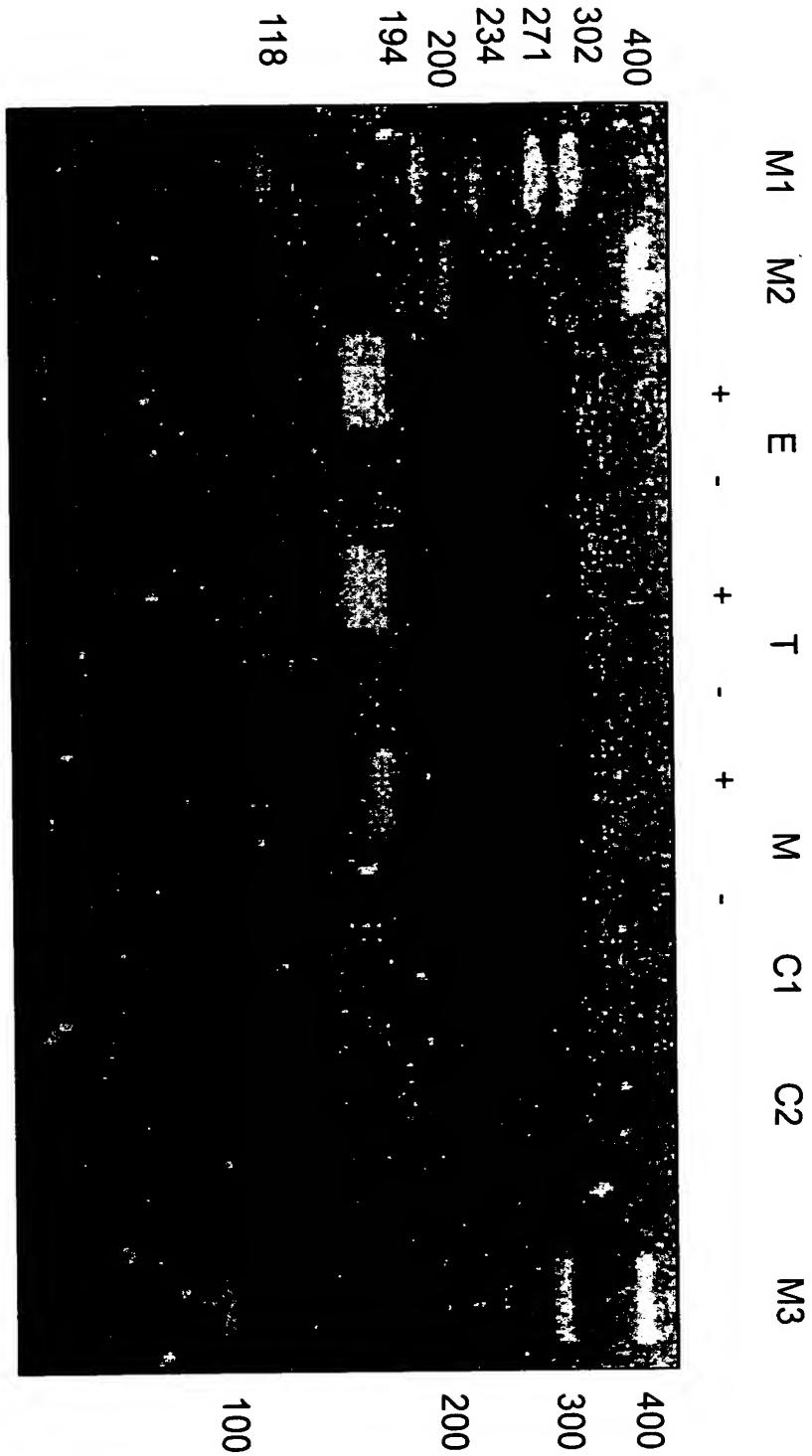


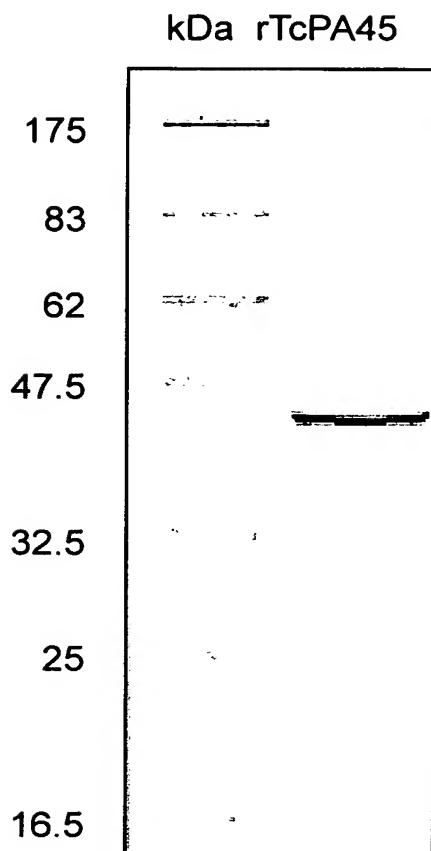
**FIG. 3A**



***FIG. 3B***

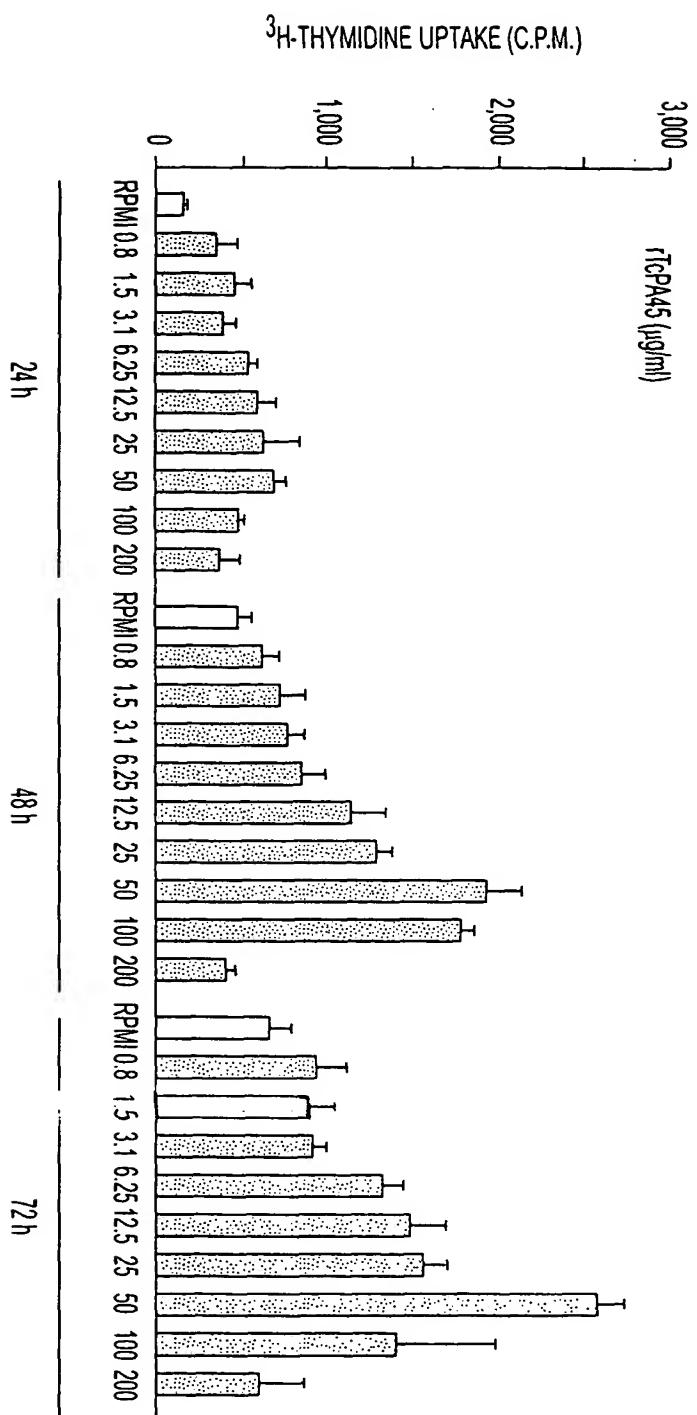
**FIG. 3C**

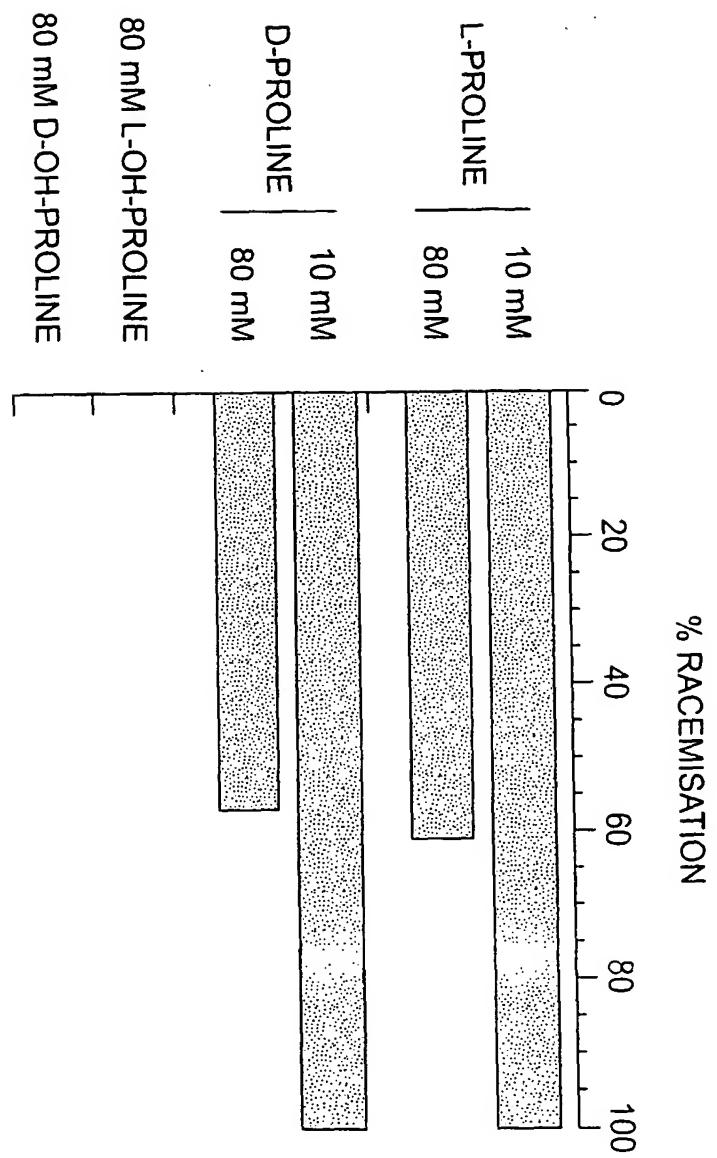




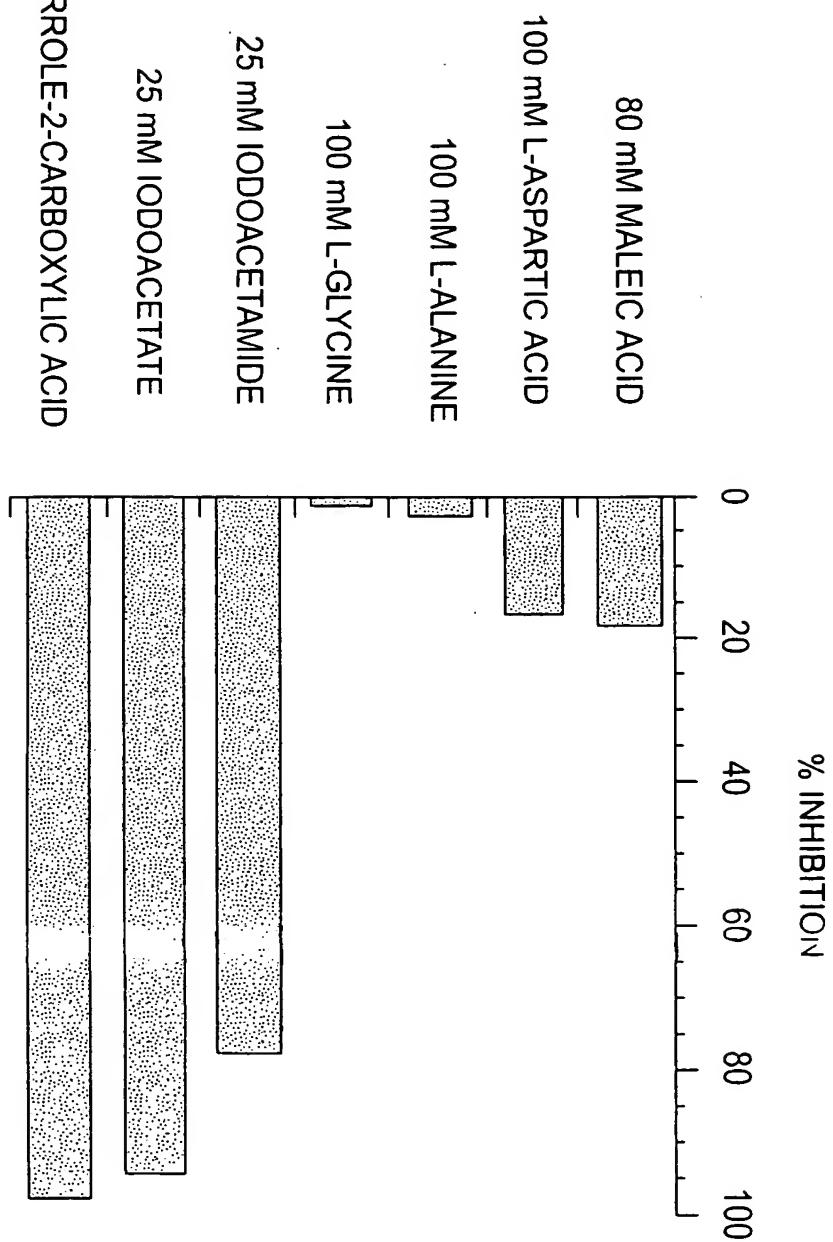
**FIG. 4A**

**FIG. 4B**

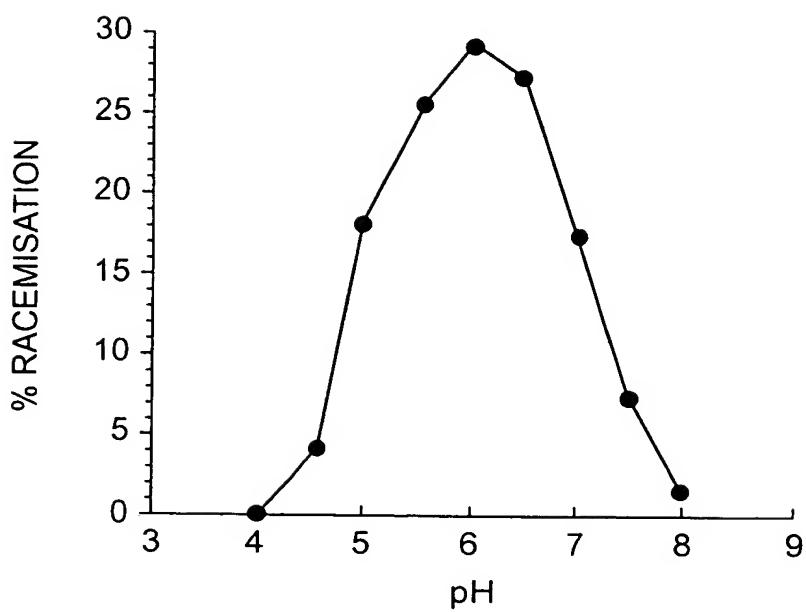




**FIG. 4C**



**FIG. 4D**

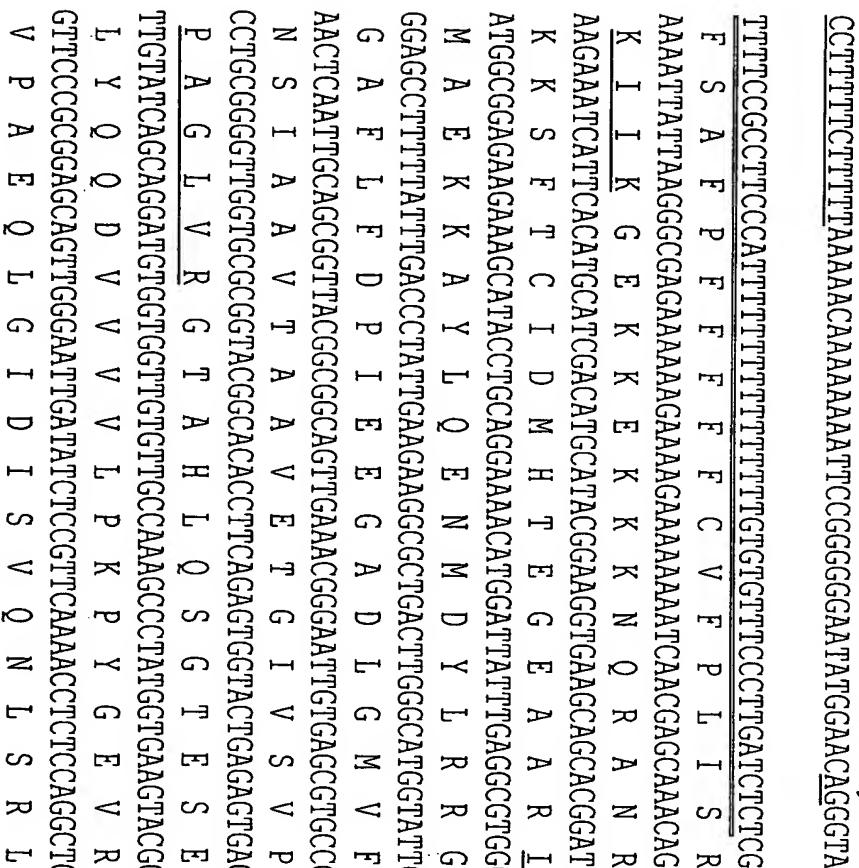


**FIG. 4E**

POLYPYRIMIDINE RICH REGION

SPLICE LEADER  
ACCEPTOR SITES

SIGNAL

CCTTTTCTTTAAACAAAAATTCCGGGGGATATGGAACAGGGTATAGGCTAAAGTGTCTGTC<sub>AAACAAA</sub>TTTT  
  
TTTCCGCCTTCCCATTTTTTTGTGTTCCCTGATCTCGAACAGGGCAGGAAGCTTCTGTTGACCAAAATTT  
F S A F P F F F F C V F P L I S R T G Q E K L L F D Q K Y  
AAAATTTAAGGGCAGAAAGAAAAGAAAAAAATCACGAGCAAACAGGAGAGACACCAACAAAGGAAATTGCGATT  
K I I K G E K K K N Q R A N R R E H Q Q K R E I M R F  
AGGAATCATTCACATGCATCGACATGCATACGGAAAGGTGAAGCAGCACGGATTGTGACGAGTGGTTGCCACACATCCAGGTCCAAT  
K K S F T C I D M H T E G E A A R I V T S G L P H I P G S N  
ATGGCGGAGAAAGCATACCTGCAGGAACATGGATTATTGAGGCCACGGTGGCATAATGCTGGAACACCACGGTGGCATGGATATGTT  
M A E K K A Y L Q E N M D Y L R R G I M L E P R G H D D M F  
GGAGCCTTTATTGACCTATGAAAGGCCGTGACTGGCATGGTATTICATGGATACGGGGCTATTAAATATGTTGGACAT  
G A F L F D P I E E G A D L G M V F M D T G G Y L N M C G H  
AACTCAATTGCAGGGTTACGGGGCAGTTGAAACGGGAATTGTGAGGGTGGGGGAAAGCCACAAATGTTGGTGTCCGGACACA  
N S I A A V T A A V E T G I V S V P A K A T N V P V V L D T  
CCTGGGGGTGGTGCGGGTACGGCACACCTCAGAGTGGTACTGAGAGTGGTCAAATGCGAGTATTCAATGTACCTCATT  
P A G L V R G T A H L Q S G T E S V S N A S I I N V P S F  
TTGTATCAGCAGGATGTGGTGGTGTGCCAAAGCCCTATGGTAAGTACGGGTGATATTGCAATTGGAGGCAATTTCGCCATT  
L Y Q Q D V V V V L P K P Y G E V R V D I A F G N F F A I  
GTTCGGCGGAGCACTGGGAATTGATATCTCCGTCACACCTCTCCAGGGTGCAGGAGGAGAACTCTGCGTACTGAATCAAT  
V P A E Q L G I D I S V Q N L S R L Q E A G E L L R T E I N

**FIG. 5A**

CGCAGTGTGAAGTTCAAGCACCCCTCAGCTCCCCATATAACACTGTGGACTGTGTGAGATATCGGTCGCCAACGAAACCCGGAGCA 970  
R S V K V Q H P Q L P H I N T V D C V E I Y G P P T N P E A 312  
AACTACAAGAACGTTGATATTGGCAATGCCAGGGATGCCCTCCATGTGGACAGGCCAACAGATGCCAACACTTAT 1060  
N Y K N V V I F G N R Q A D R S P C G T G T S A K M A T L Y 342  
GCCAAAGGCCAGCTGGCATCGGAGACTTTGTGTACGGAGAGCATACTCGGCTCACTCTCCAGGGAGGGTACTTGGGAGGGAGGA 1150  
A K G Q L R I G E T F V Y E S I L G S L F Q G R V L G E E R 372  
ATACCGGGGCTGAAGGTGCCGGTGACCAAAGATGCCAGGAAGGGATGCTCGTTAACGGCAGAAATTACTGAAAGGTTTATCATG 1240  
I P G V K V P V T K D A E E G M L V V T A E I T G K A F I M 402  
GGTTCAACACCATGCTGTTGACCCAACGGATCCGTTAAGAACGGATTCCACATTAAGCACTGAGTAGATCTGGTAGAGCACAGAACTATT 1330  
G F N T M L F D P T D P F K N G F T L K Q 423  
GGGAACACGTTGCGAACAGGTGCTACGTTGAAGGGTATGAATGAACTGTTTTTATTATTATTATTATTAGTCATT 1420

ATATTAATTTTTTGTGTTGGGTTCAACGGTACCGGCTGGGACGGAGCGATAGGGGGACAATTGGCTTT 1510

TTTCATTTCATCTCCTACCCACCCCTGGTCCACCGGTGCCGGGGCTGTGGTGGAGGACTCTAAATCCGCACCTCGG 1600

AGGAATAACATATTCATCTGGAAATCAAAGGCAT

1651

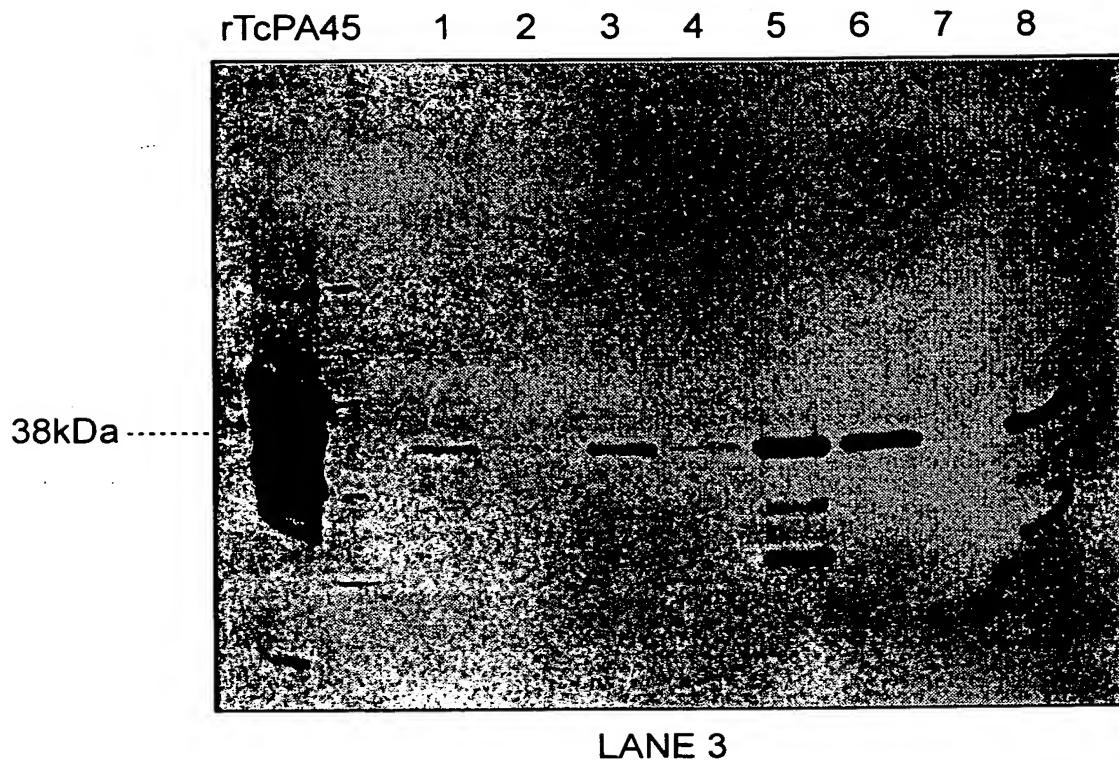
POLYADENYLATION SITE

OBS: UNDERLINED THE SEQUENCED PEPTIDES USED TO DEDUCE DEGENERATED PRIMERS FOR CLONING

NUCLEOTIDE SEQUENCE AND PEPTIDE SEQUENCE TCPA45

**FIG. 5B**

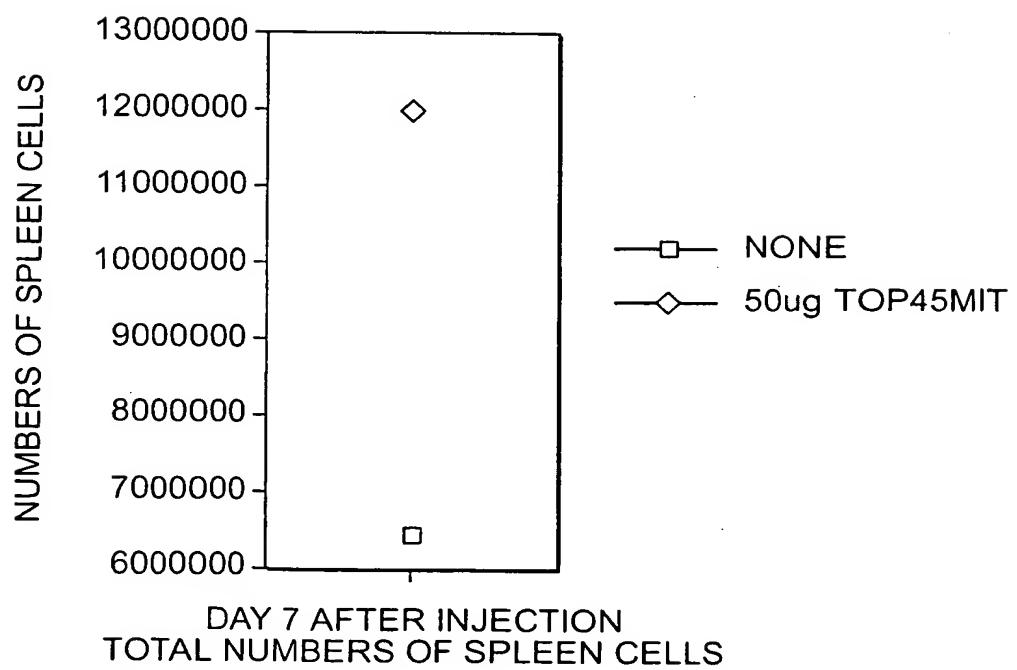
WESTERN BLOT



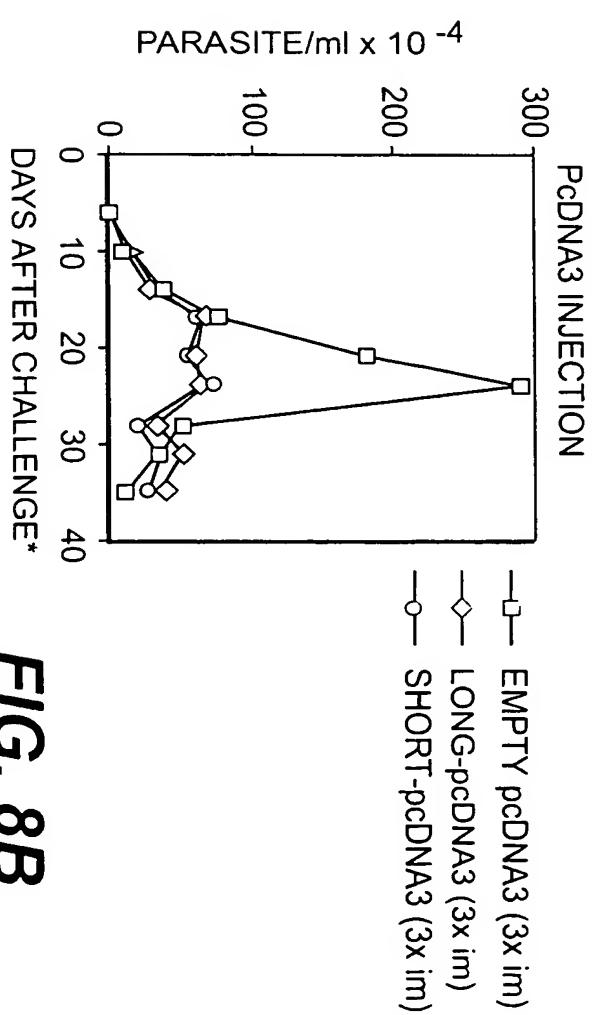
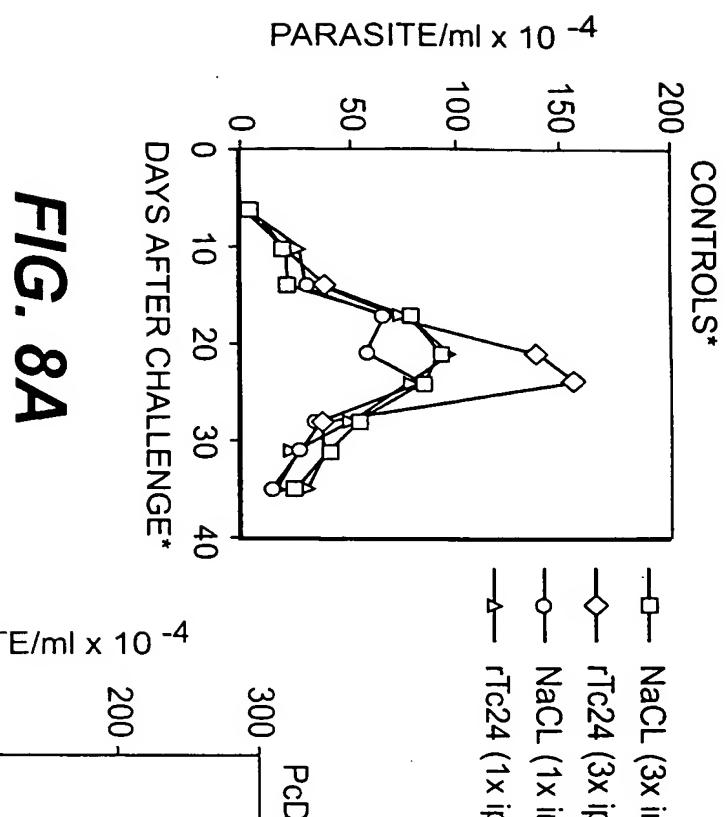
SOLUBLE FRACTION OF EPIMASTIGOTES EXTRACT (CYTOSOLIC)  
REVEALED WITH ANTIBODY DIRECTED TO rTcPA45

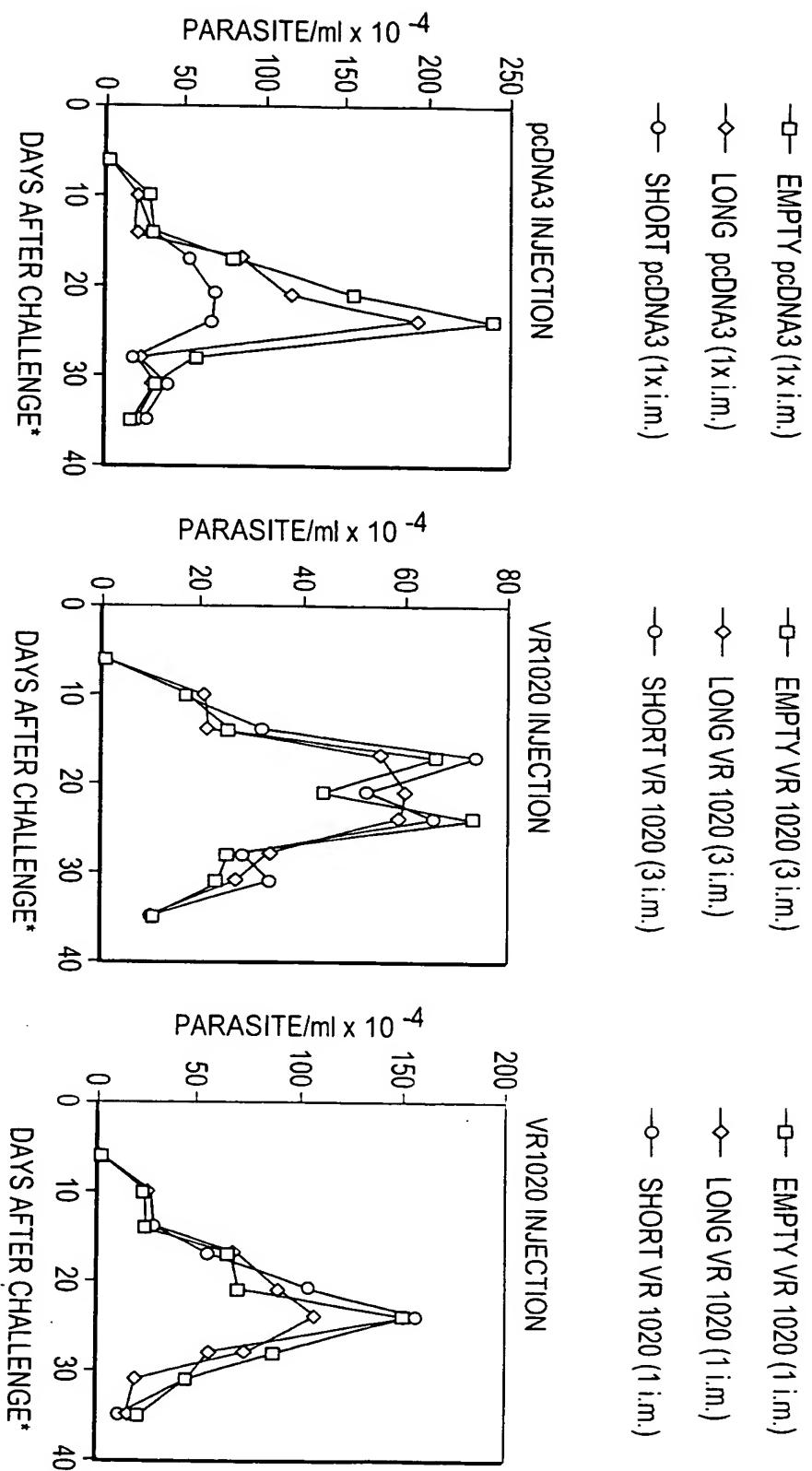
----- DEMONSTRATES THE EXISTANCE OF AN INTRACYTOPLASMIC  
FORM OF TcPA45 IN THE PARASITE

**FIG. 6**



**FIG. 7**

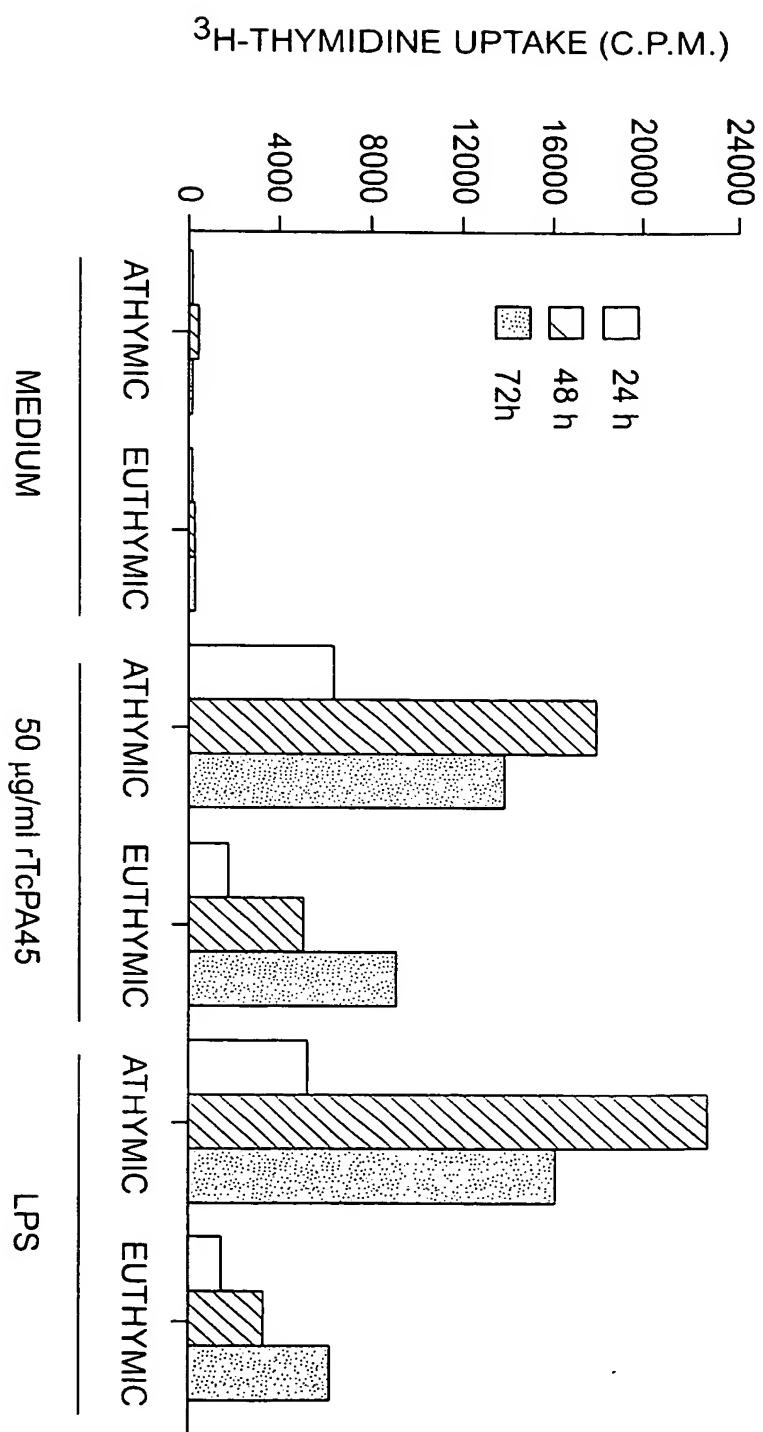




**FIG. 8C**

**FIG. 8D**

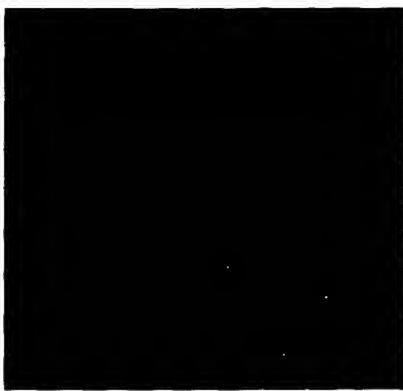
**FIG. 8E**



**FIG. 9**

Alexa-F (ab')2

Chronic serum

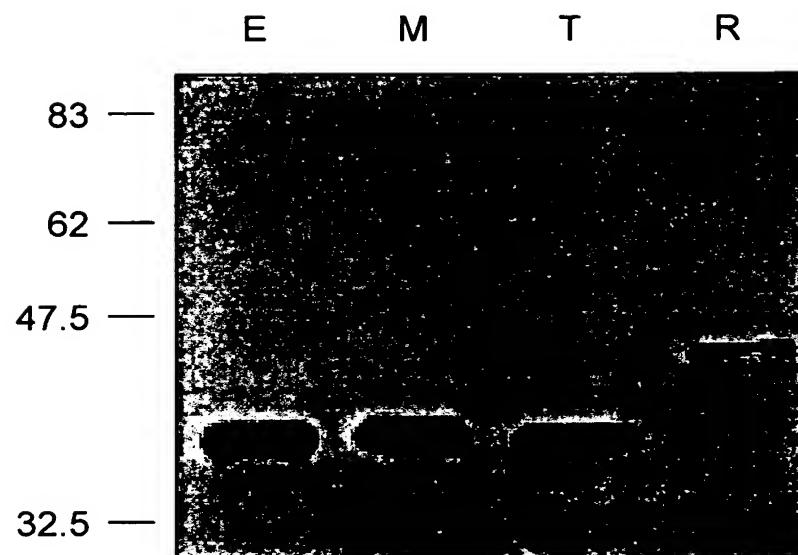


EPIMASTIGOTE

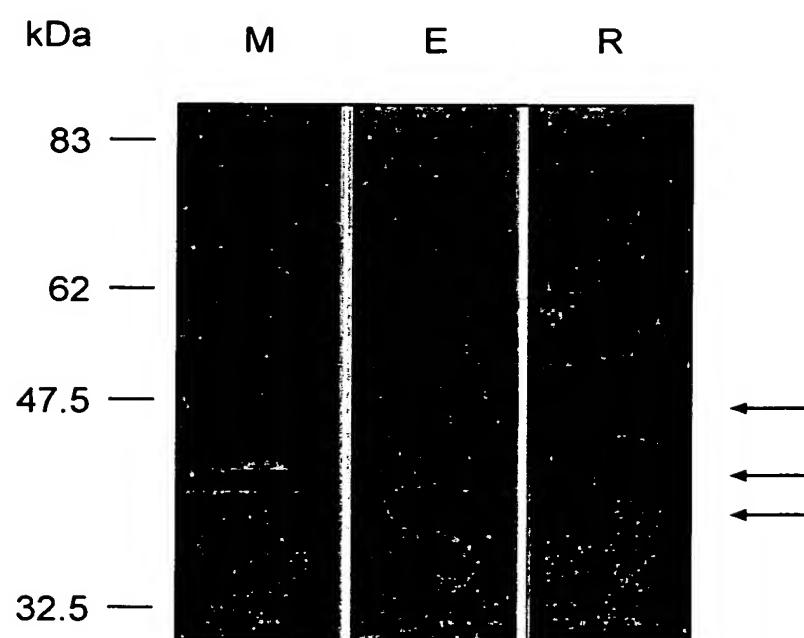
METACYCLIC

TRYPOMASTIGOTE

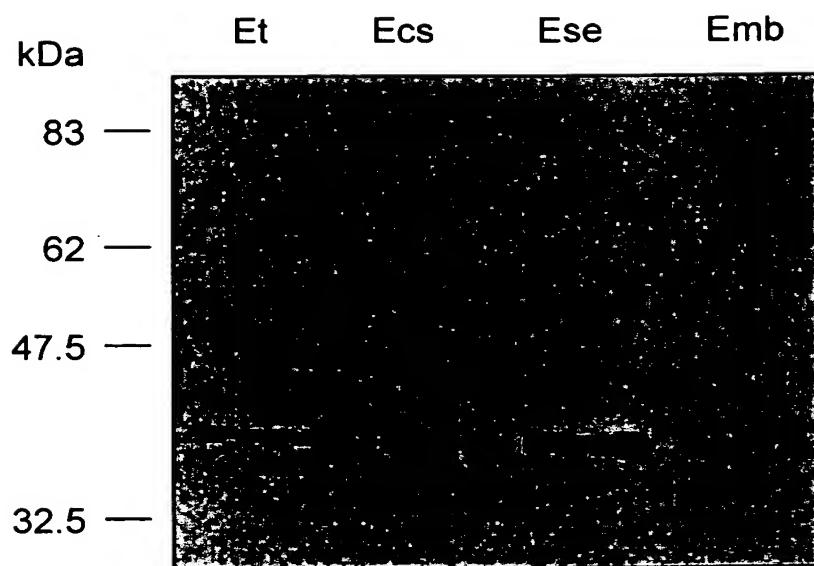
**FIG. 10A**



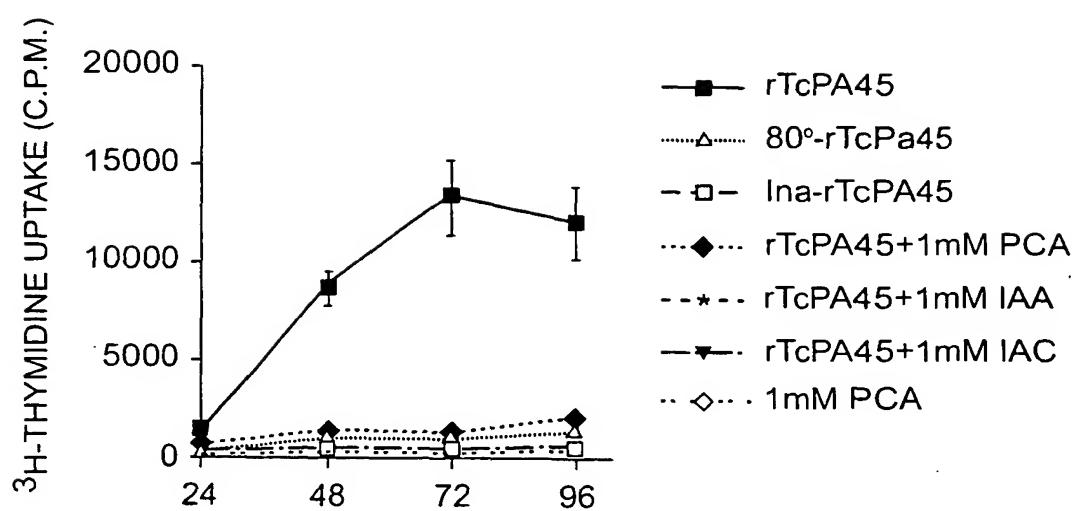
***FIG. 10B***



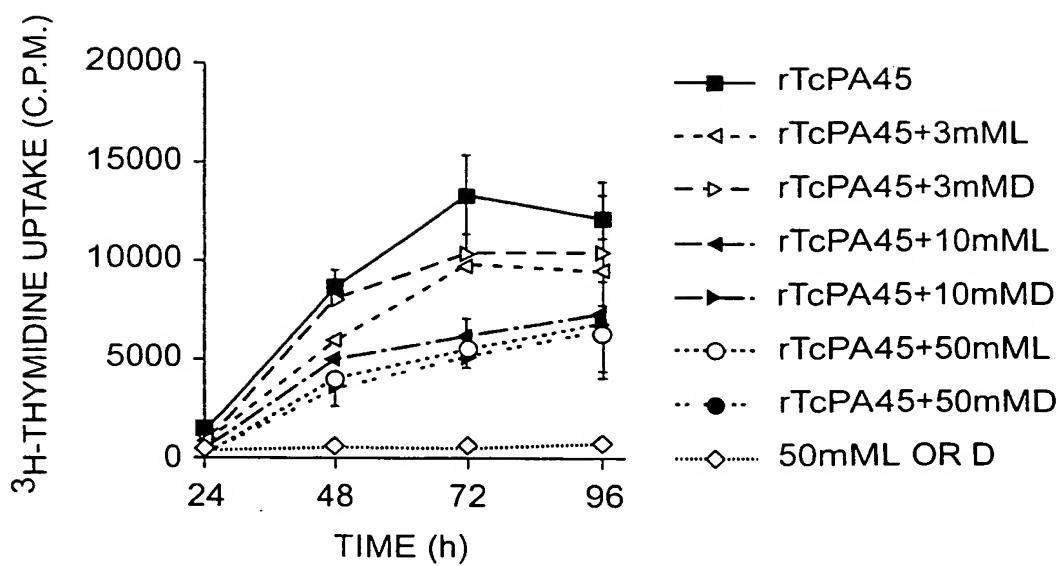
**FIG. 10C**



**FIG. 10D**

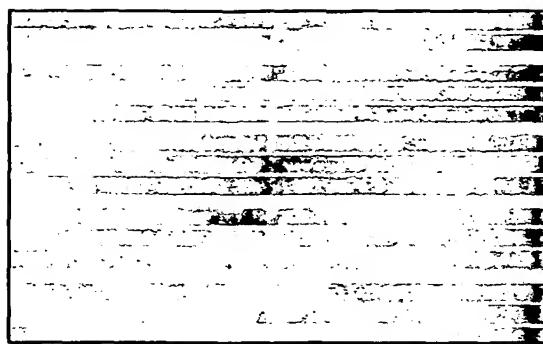


**FIG. 11A**

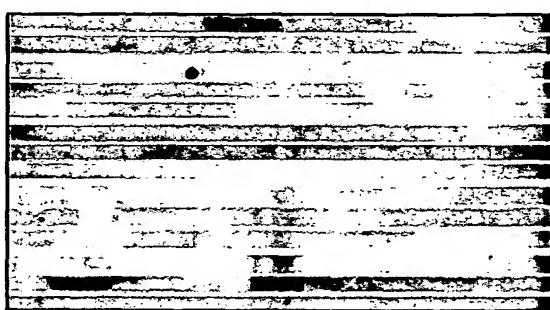


**FIG. 11B**

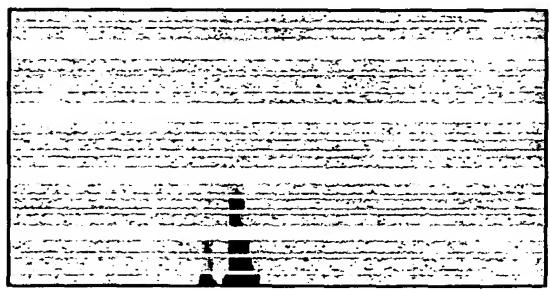
J-14



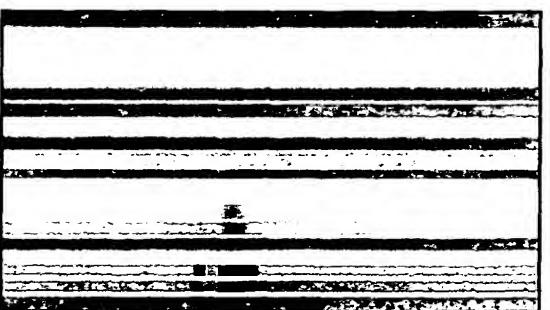
J0



J10



J21



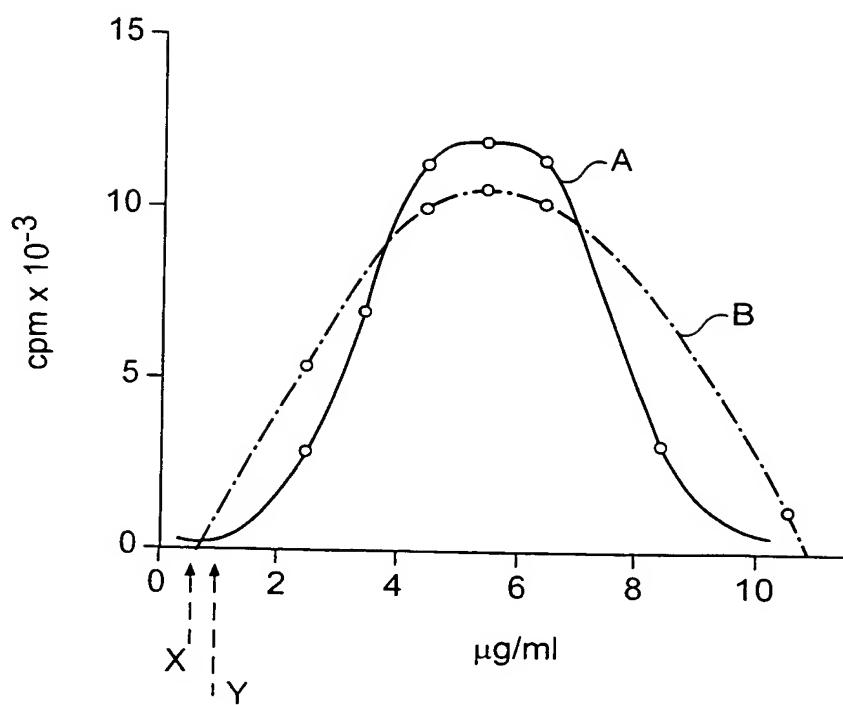
**FIG. 12**

T Y C I I  
I O C I I  
D U O S P  
E R S T

T Y C I I  
I O C I I  
D U O S P  
E R S T

T Y C I I  
I O C I I  
D U O S P  
E R S T

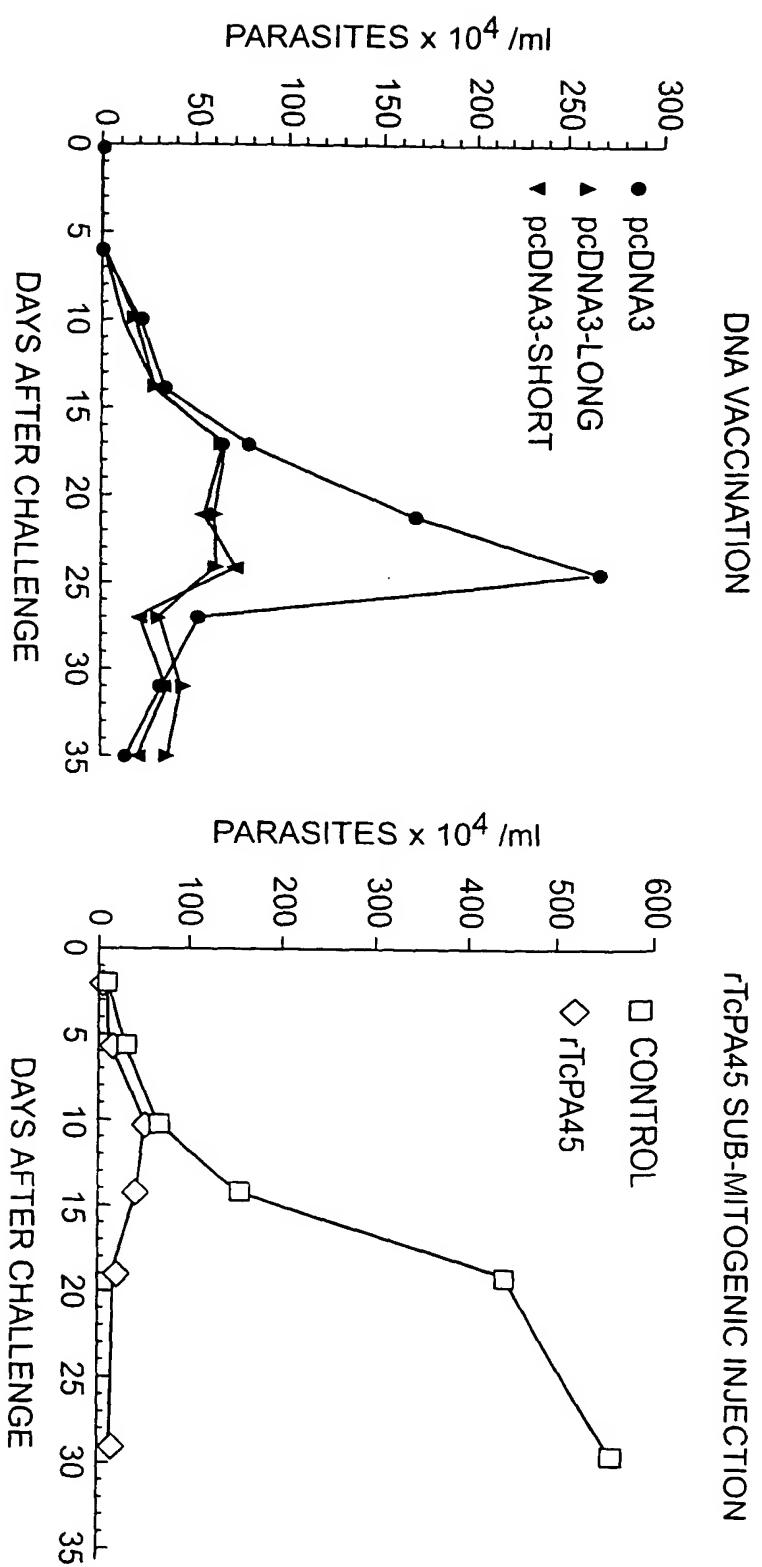
T Y C I I  
I O C I I  
D U O S P  
E R S T



**FIG. 13**

**Replacement Figure 14A and 14B  
Divisional Application of 09/725,945**

Inventors: Mihophio et al.  
Attorney Docket No. 03495-02000-02000



*FIG. 14A*

SEQ ID NO:2

TC RTGQEKL~~LFDQKYK~~KIKEKKNNQRANRREHQKREIMRFKKS 75  
TC FTCIDMHTEGEAARIVTSGLPHIPGSNMAEKKAYLQENMDYLRRGIMLEPRGHDDMFGAFLFDPIEGADLG~~MVF~~ 150  
TC MDTGGYLNMC~~GHN~~SIAAVTA~~A~~VETGIVSVPAKATNVPVLDTPAGLVRGT~~A~~HLSQ~~G~~TESEVS~~N~~ASINVPSFLYQ 225  
TC QDVVVVLPKPYGEVRVDIAGGNFAIVPAEQ~~O~~LGIDISVQNL~~S~~R~~I~~QEA~~G~~ELL~~R~~T~~E~~INRSVKVQH~~P~~LPHINTVDC 300  
TC VEIYGPPTNPEANYKNVWIFGNQADR SPCGT GT~~S~~AKM~~A~~TLYAKGQ~~Q~~LRIGETFVYESILGSLFQGRV--LGEE 371  
TC R~~I~~PGVKVPVTKDAE~~E~~GM~~L~~VVTAEITGKA~~F~~IMG~~F~~NTMLFDPTDPFKNGFTLKQ\* 423

**FIG. 15**

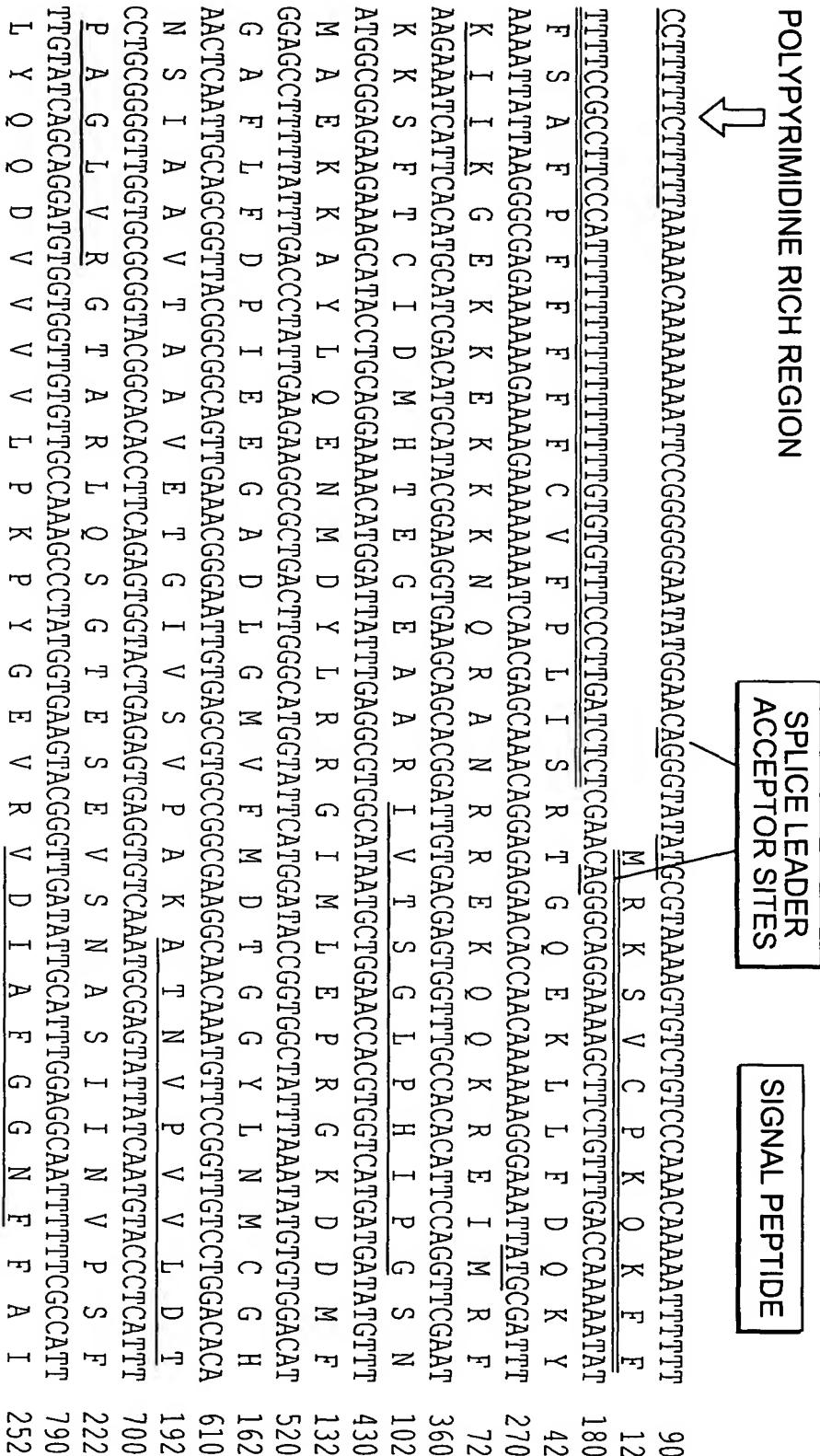
SEQ ID NO:4

Tc	MRFKKS	75
Tc	FTCIDMHTEGEARIVTSGLPHIPGSNMAEKAYLQENMDYLRRGIMLEPRGHDDMFGAFLFDPIEEGADLGMVF	150
Tc	MDTGGYLNMCGHNSIAAVTAAVETGIVSVPAKATNVPVVLDTPAGLVRGTAHLQSGTESEVSNASIINVPSFLYQ	225
Tc	QDVVVVLPKPYGEVR <u>V</u> DIAFGGN <u>F</u> AIVPAEQLIGIDI SVQNLISRLQEAGEELIRTEINRSVKVQHQLPHINTVDC	300
Tc	VEIYGPPTNPEANYK <u>N</u> WIFGNRQADR <span style="border: 1px solid black; padding: 2px;">SPCGT</span> GTSAKMATLYAKGQLRIGETFVYESILGSLFQGRV--LGEE	371
Tc	RIPGVKVVPVTKDAEEMLVVTAETITGKAFIMGFNTMLFDPTDPFKNGFTLKQ*	423

**FIG. 16**

POLYPYRIMIDINE RICH REGION

SEQ ID NO:7



**FIG. 17A**

GTTCCCGGGAGCAGTGGAAATTGATATCTCCGTTCAAACCTCTCCAGGCTGCCAGGAGAAGACTCTCGTACTGAATCAAT 880  
V P A E Q L G I D I S V Q N L S R L Q E A G E L L R T E I N 282  
CGCAGTGTGAAGGTTCACGCCCTCACCTGCCATATACTGAGATACGGTCCCAACGGAGGCA 970  
R S V K V Q H P Q L P H I N T V D C V E I Y G P P T N P E A 312  
AACTACAAGAACGTTGTGATATTGCAATGCCAGGGATCGCTCTCCATGTGGACAGGCACCAGGCCAACATGGCAACACTTAT 1060  
N Y K N V V I F G N R Q A D R S P C G T G T S A K M A T L Y 342  
GCCAAAGGCCAGCTCGCATGGAGAGACTTTGTGTACCGAGAGCATACTCGGCTCACTCTCAGGGCAGGGTACTGGGGAGGCGA 1150  
A K G Q L R I G E T F V Y E S I L G S L F Q G R V L G E E R 372  
ATACCGGGGGTGAAGGTCGGTACCAAAGATGCCGAGGAAGGGATGCTCTGTAAAGGCACAAATTACTGAAAGGCTTTATCATG 1240  
I P G V K V P V T K D A E E E G M L V V T A E I T G K A F I M 402  
GCTTTCACACCATGCTTTGACCAACGGATCCGTTAAGAACGGATTACATTAAAGCACTAGATCTGGTAGACCCACAGAACATT 1330  
G F N T M L F D P T D P F K N G F T L K Q \* 423  
GGGGAACACGTGCGAACAGGTGCTACGTGAAGGGTATGAATGAACTGGTTTTTATTATTATTATTATTAGTCATT 1420  
ATTATAAACATTTCATTCATTTCATATCTGGAAATAAGGCAT 1510  
TTCATTTCATCTCCATACCCAAACCCCTGGTTCCACCGGTCGGGGGGCTCTGGGTGGAGGACTCTAAATCCGCACCTCGG 1600  
AGGAATAAACATATTCAATTCAATCTGGAAATAAGGCAT 1651

**POLYADENILATION SITE**

Obs: UNDERLINED THE SEQUENCED PEPTIDES USED TO DEDUCE DEGENERATED PRIMERS  
FOR CLONING

(b) NUCLEOTIDE SEQUENCE AND PEPTIDE SEQUENCE TcPA45

**FIG. 17B**

SEQ ID NO:8

<u>ATGGCTAAAGTGTCTCCCCAACCAAAATT</u>	90
M R K S V C P K O K F F	12
<u>TTTCCGCCTTCCCATT</u> <u>TTTGTGTTCCCTGATCTCGAACAGGCAGGAAAGCTCTGTTGACCAAAAT</u>	180
F S A F P F F F C V F P L I S R T G Q E K L L F D Q K Y	42
<u>AAATTATAAGGCCGAGAAAAAGAAAAAGAAAAATCACCGACAAACAGGAGAACACCAACAAAAGGAATT</u> <u>TGCGATT</u>	270
K I I K G E K K E K K N Q R A N R R E H Q Q K R E I M R F	72
<u>AAGAAATCATCACATGCATGCACATGCCATACCGAAGGTGAAGCACCACGGATTGTGACGACTGTTGCCACACATCCAGGTCGAAT</u>	360
K K S F T C I D M H T E G E A A R I V T S G L P H I P G S N	102
<u>ATGCCGGAGAGAACGATACCTGCAGGAAACATGGATTATTGAGGCCATATACTGGAAACCACGTGGCATGATGATATGTT</u>	430
M A E K K A Y L Q E N M D Y L R R G I M L E P R G H D D M F	132
<u>GGAGCCTTTATTTGACCTATTGAAAGAGGCCGTGACTTGGCATGGTATCATGGATACCGGGCTATTAAATATGTTGACAT</u>	520
G A F L F D P I E E G A D L G M V F M D T G G Y L N M C G H	162
<u>AACTCAATTGAGCGGTACGGCGCAGTGAAACGGAATGTGAGCGTGGCGAGGCCAACAAATGTCGGTTGCTGGACACA</u>	610
N S I A A V T A A V E T G I V S V P A K A T N V P V V L D T	192
<u>CCTGGGGGTGGCGCGTACGGCACACCTCAGAGTGGTACTGAGAGTGGTCAAATGGAGTATTATCAATGTACCCATT</u>	700
P A G L V R G T A H L Q S G T E S E V S N A S I I N V P S F	222
<u>TTGTATCAGCAGGATGGTGGTGTGTTGCAATGGGAATTGATATCTCCGTC</u> <u>AAACCTCTCCAGGCTGCAGGAGCAGGAGAACTCTGCGTACTGAATCAAT</u>	790
L Y Q Q D V V V L P K P Y G E V R V D I A F G G N F F A I	252
<u>GTTCCCGCGGAGCAGTGGAAATTGATATCTCCGTC</u> <u>AAACCTCTCCAGGCTGCAGGAGCAGGAGAACTCTGCGTACTGAATCAAT</u>	880
V P A E Q L G I D I S V Q N L S R L Q E A G E L L R T E I N	282
<u>CGCAGTGTGAAGGTTCACGCACCCCTAGCTGCCCATATTAACTGTTGACCTGGTGTGAGATATACGGTCCGCAACGAAACCCGGAGGCA</u>	970
R S V K V Q H P Q L P H I N T V D C V E I Y G P P T N P E A	312

**FIG. 18A**

Divisional Application of 09/725,945  
Inventors: Minoprio et al.  
Attorney Docket No. 03495-0200-02000

AACTACAAAGAACGGTGTGATATTGGCAATGCCAGGGATCGCTCTCCATGGACAGGCACCGGCCAAGATGGCAACTTTAT 10600  
 N Y K N V V I F G N R Q A D R S P C G T G T S A K M A T L Y 342  
 GCCAAAGGCCAGCCTCGCATCGGAGAGACTTTGTGTACCGAGAGCATACTCGGCTCACTTCCAGGGCAGGGTACTGGGAGGAGCGA 11500  
 A K G Q L R I G E T F V Y E S I L G S L F Q G R V L G E E R 372  
 ATACCGGGGTGAAGGTGCCGGTGACCAAAGATGCCAGGGAAAGGATGCTCGTGTAAACGGCAGAAATTACTGGAAGGGTTTATCATG 12400  
 I P G V K V P V T K D A E E G M L V V T A E I T G K A F I M 402  
 GGTTCACACCATGCTGTTGACCCAAAGGATCCGTTAACGAGATCACATTAAACGAGTAGATCTGGTAGAGCACAGAACTATT 13300  
 G F N T M L F D P T D P F K N G F T L K Q \* 423  
 GGGAACACCGTGGAACAGGGTGTGCTACGTGAAGGGTATGAATGAATCGTTTTTATTATTATTATTAGTCATT 14200

ATTATTAATTTTTGTTGGGTTCAACGGTACCGCGTGGAGCAGGAAGCGATAGGCCGACAATTTGCTTTAT 15100

TTTCATTTCATCTTCCCTACCCAACCCCCTGGTCCACCGGTGCGGGGCTTGTGGTGGAGGACTTAATCCGCACCTCGG 16000

AGGAATAACATATTCAATTTCATATCTTGGAAATCAAAGGCAT  
1651

1651

## POLYADENYLATION SITE

**Obs: UNDERLINED THE SEQUENCED PEPTIDES USED TO DEDUCE DEGENERATED PRIMERS  
FOR CLONING**

NUCLEOTIDE SEQUENCE AND PEPTIDE SEQUENCE TcPA45

**FIG. 18B**

SEQ ID NO:9

CGAACAGGGCAGGAAAGCTCTGTTGACCAAAAT	270
R T G Q E K L I F D Q K Y	72
AAAATTAAAGGGCGAGAAAAAGAAAAAAATCACCGAGAACACCAACAAAAAGGAAATT <u>TGCCGATT</u>	360
K I I K G E K K E K K N Q R A N R R E H Q Q R R E I M R F	102
AAGGAATCATCACATGCATCGACATGCATAACGGAAAGGTGAAGCAGCAGGATGTGACCAGTGGTTGCCACACATCCAGGTTCGAAT	430
K K S F T C I D M H T E G E A A R I V T S G L P H I P G S N	132
ATGGCGGAGAGAACGATAACCTGCAGGAAACATGGATTATTGAGGCCATATGCTGGAACACGGGGTCATGATGATATGTT	520
M A E K K A Y L Q E N M D Y L R R G I M L E P R G H D D M F	162
GGAGCCTTTATTGACCTATGAGAACGGCCTGACTGGCATGGTATCATGGATAACGGGGCTATTAAATATGTTGGACAT	610
G A F L F D P I E E G A D L G M V F M D T G G Y L N M C G H	192
AACTCAATGCAGGGTACGGCGCAGTTGAACGGGAATGTGAGCGTGGCGAACGACAATGTCCGGTGTCCGGACACA	700
N S I A A V T A A V E T G I V S V P A K A T N V P V V L D T	222
CCTGGGGGTGGCGGGTACGGCACACCTCAGAGTGGTACTGAGACTGAGGTGTCAAATGGAGTATTATCAATGTACCCATT	790
P A G L V R G T A H L Q S G T E S E V S N A S I I N V P S F	252
TTGTATCAGCAGGATGGTGGTGTGTTGCCAAAGCCCTATGGTAAGTACGGGTGATATTGCAATTGGAGGCAATTTCGCCATT	880
L Y Q Q D V V V L P K P Y G E V R V D I A F G G N F F A I	282
GTTCCCGGGAGCAGTGGAAATTGATATCTCCGTCACAAACCTCTCCAGGGTGCAGGGAGGAGACTCTGGTACTGAATCAAT	970
V P A E Q I D I S V Q N L S R L Q E A G E L L R T E I N	312
CGCAGTGTGAAGGTTCAACACCCCTCAGCTGCCCATATTAACACTGTGGACTGTGAGATATCGGTCCGCCAACGAAACCGGAGGCA	1060
R S V K V Q H P Q L P H I N T V D C V E I Y G P P T N P E A	342
AACTACAAGAACGTTGTGATATTGGCAATGCCAGGGCATGCCCTCCATGTGGCACAGGCCAACAGTGGCAACACTTAT	1150
N Y K N V V I F G N R Q A D R S P C G T G T S A K M A T L Y	372

**FIG. 19A**

New Figure 19B  
Divisional Application of 09/725,945  
Inventors: Minoprio et al.

Divisional Application of 09/725,945  
Inventors: Minoprio et al.  
Attorney Docket No. 03495-0200-02000

GCCAAAGGCCAGCTTCGCATCGGAGAGACTTTGTGTACGGAGGCATACTCGGCTCACTTCCAGGGCAGGGTACTGGGAGGGCGA 12400  
A K G Q L R I G E T F V Y E S I L G S L F Q G R V L G E E R 402  
 ATACCGGGGTGAAGGTGCCGGTGACCAAAGATGCCGAGGAAGGGATGCTCGTTGTAACGGCAGAAATTACTGGAAAGGCCATTATCATG 13300  
 I P G V K V P V T K D A E E G M L V V T A E I T G K A F I M 423  
 GGTTCACACACCATGCTGTTGACCCAACGGATCCGTTAACGAGGATTCACATTAACCGAGTAGATCTGGTAGAGCACAGAACTATT 14200  
 G F N T M L F D P T D P F K N G F T L K Q \* .  
 GGGAACACGTGCCAACAGGTGCTACGTGAAGGGTATGAATGAATCGTTTTTATTTTATTTATAGTGCTT 15100

ATTATAATTGTTGGGTTCAACGGTACCGCTGGACAGGAAGCGATAGCGCCGGACAATTGCTTTAT 1600

AGGAATAACATATTCAATTTCATATCTTGGAAATCAAAGGCAT

## POLYADENYLATION SITE

**Obs: UNDERLINED THE SEQUENCED PEPTIDES USED TO DEDUCE DEGENERATED PRIMERS  
FOR CLONING**

NUCLEOTIDE SEQUENCE AND PEPTIDE SEQUENCE TcPA45

FIG. 19B

SEQ ID NO:10

SIGNAL PEPTIDE

ATGCGTAAAGTGTCTGTCCAAACAAATTTTT

TTTTCGGCTTCCATTTTTTTTTGTTGTTCCCTTGATCTCT

NUCLEOTIDE SEQUENCE OF SIGNAL SEQUENCE TcPA45

**FIG. 20**

SEQ ID NO:11

	ATGCCATT			360
	M	R	F	102
AAGAAATCATTACATGCCATGCACATGCCAACGGGATTGTGACCGACCGATTGCCACACATTCCAGGTTCGAAT				430
K K S F T C I D M H T E G E A A R I V T S G L P H I P G S N				132
ATGCCGGACAAGCATACCTGCAGGAAACATGGATTATTGAGGGCTGCATAATGCTGGAACACGCTGGCATGATGATATGTTT				520
M A E K K A Y L Q E N M D Y L R R G I M L E P R G H D D M F				162
GGACCCCTTTATTGACCCATTGAAGAAGGGCTGACTTGGCATGGTATTCAATGGATACCGGTGGCTATTAAATATGTGTGACAT				610
G A F L F D P I E E G A D L G M V F M D T G G Y L N M C G H				192
AACTCAATTGCAAGCGGTACGGCGCACACCTTCAGAGTGGTACTGAGAGTGAGGTGTCAAATGGAGTATTCAATGTACCCCTCATTT				700
N S I A A V T A A V E T G I V S V P A K A T N V P V V L D T				222
CCTGGGGGTGGTGCACGGTACGGCACACCTTCAGAGTGGTACTGAGAGTGAGGTGTCAAATGGAGTATTCAATGTACCCCTCATTT				790
P A G L V R G T A H I Q S G T E S E V S N A S I I N V P S F				252
TGTATCAGCAGGATGTGGTGGTGTGCCAACGCCATTGGTAAGTACGGGTGGATATTGCCATTGGGCAATTTCGCCATT				880
L Y Q Q D V V V L P K P Y G E V R V D I A F G G N F F A I				282
GTCCCCGGAGCAGTTGGATTGATATCTCCGTTCAAACCTCCAGGCTGCAGGAGGAGAACTTCTGGTACTGAATCAAT				970
V P A E Q L G I D I S V Q N L S R L Q E A G E L L R T E I N				312
CGCAGTGTGAAGGTTCAAGCACCCCTCAGCTGCCATTAAACTGTGGACTGTGTGAGATATCGGTCCGCCAACGAAACCGGAGGCA				1060
R S V K V Q H P Q L P H I N T V D C V E I Y G P P T N P E A				342
AACTACAAGAACGTTGTGATATTGGCAATGCCAGGGATGCCCTCCATGTGGACAGGCCAACGCGCAAGATGGCAACACCTTAT				1150
N Y K N V V I F G N R Q A D R S P C G T G T S A K M A T L Y				372
GCCAAAGGCCAGCTCGCATCGGAGAGACTTTGTGTACGAGAGCATACTCGGCTCACCTCCAGGGCAGGGTACTGGGAGGAGCGA				1240
A K G Q L R I G E T F V Y E S I L G S I F Q G R V L G E E R				402

**FIG. 21A**

ATACCGGGGTGAAGGTGCCGGCACCAAAGATGCCGAGGAAGGGATGCTCGTGTAAACGGCAGAAATTACTGGAAAGGCTTTATCATG 1330  
I P G V K V P V T K D A E E G M L V V T A E I T G K A F I M 423  
GCTTTCAACACCATGCTGTTGACCCAACGGATCCGTTAACGAGTAGATCTGGTAGAGCACAGAACTATT 1420  
G F N T M L F D P T D P F K N G F T L K Q \*  
GGGAAACACGTGCGAACAGGTGCTGCTACGTGAAGGGTATTGAATCGTTTTTATTATTATTATTATTAGTCATT 1510  
  
ATTATAAATTTTTGGGTTCAACGGTACCGCTGGGAGCAGGAAGCGATAGGCCGACAATTGGCTTTAT 1600  
TTTCATTTCATCTCCTACCCAACCCCTTGTTCCACCGGTGGGGGGTCTGGGGAGGACTCAAATCCGCACCTCGG 1651  
AGGATAAACATATTCAATTTCATATCTGGAAATCAAAGGCAATT

**FIG. 21B**